OIPE

#2

ENTERED

RAW SEQUENCE LISTING   DATE: 07/24/2001
PATENT APPLICATION: **US/09/900,237**   TIME: 10:13:55

Input Set : **A:\BB1170 US CIP Seq Listing.txt**
Output Set: **N:\CRF3\07242001\I900237.raw**

ρ$

```
       2 <110> APPLICANT: Allen, Stephen
       4 <120> TITLE OF INVENTION: Plant Cellulose Synthases
       6 <130> FILE REFERENCE: BB1170 US CIP
C-->   8 <140> CURRENT APPLICATION NUMBER: US/09/900,237
C-->   9 <141> CURRENT FILING DATE: 2001-07-06
      11 <150> PRIOR APPLICATION NUMBER: 60/092,844
      12 <151> PRIOR FILING DATE: 1998-07-14
      14 <150> PRIOR APPLICATION NUMBER: PCT/US99/15871
      15 <151> PRIOR FILING DATE: 1999-07-13
      17 <150> PRIOR APPLICATION NUMBER: 09/720383
      18 <151> PRIOR FILING DATE: 2000-12-21
      20 <160> NUMBER OF SEQ ID NOS: 33
      22 <170> SOFTWARE: Microsoft Office 97
      24 <210> SEQ ID NO: 1
      25 <211> LENGTH: 1221
      26 <212> TYPE: DNA
      27 <213> ORGANISM: Hordeum vulgare
      29 <400> SEQUENCE: 1
      30 gcacgaggat attcttactg ggtttaaaat gcacgcaaga ggttggatat caatctactg    60
      31 catgccacca cgaccttgtt tcaagggttc tgcgccaatc aatctctctg accgtctcaa   120
      32 tcaagttctc cggtgggctc ttgggtcagt tgaaattctg tttagcagac attgtcctat   180
      33 ctggtacaat tacggtgggc ggttgaaact tctggagagg atggcttaca tcaacaccat   240
      34 tgtttatcca ataacatccc ttccacttat cgcctattgt gtgcttcctg ctatctgtct   300
      35 cctcaccaac aaatttatca ttcccgagat cagtaactat gctgggatgt ctttattct   360
      36 tatgtttgcc tccatctttg ccacgggtat attggagctg cgatggagtg gtgtcggcat   420
      37 cgaggactgg tggagaaacg agcagttctg ggttattggt ggcacatctg cccatctttt   480
      38 cgcagtgttc cagggtctgc tgaaggtgtt ggccgggatt gacaccaact tcacggttac   540
      39 ctcgaaggca aacgacgagg atggcgattt tgctgagtta tacgtgttca agtggaccag   600
      40 tctcctcatt cctccgacca ccgtccttgt gattaacctg gtgggcatgg tggcaggcat   660
      41 atcatatgcc atcaacagcg gttaccagtc ttggggtcca ctcttcggaa agctcttctt   720
      42 ctcaatctgg gtgatcctcc atctctaccc cttcctcaag ggtctcatgg ggaagcagaa   780
      43 ccgcacgcca accatcgtca ttgtttggtc catcctccta gcctccatct tctccctcct   840
      44 gtgggtgaag atcgaccctt tcatatccga tacccagaaa gccgtcgcca tggggcagtg   900
      45 tggcgtcaac tgctgatcgg cgccgaagag tatctgcccc cctcgtgtaa ataccggagg   960
      46 gggttggatg ggattttgtt gttgtagatg aagacggagt tttatgtaag ttattattgc  1020
      47 cccttcgtgc tgagaagcac aaaccgtgaa gcctacgaaa cctgcagcgt acattgtgat  1080
      48 ttttttctcc ttttcttttc atctgtgata cctgttgttt cttcttagag tatattatgt  1140
      49 cagaacgtat ctatagttct atacacacta tgacaccaac tatttatata aggcagctgt  1200
      50 tgcatcaact cttctgcaaa a                                             1221
      52 <210> SEQ ID NO: 2
      53 <211> LENGTH: 304
      54 <212> TYPE: PRT
      55 <213> ORGANISM: Hordeum vulgare
      57 <400> SEQUENCE: 2
      58 His Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Ile
      59  1               5                  10                  15
      61 Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser Ala Pro
```

RAW SEQUENCE LISTING   DATE: 07/24/2001
PATENT APPLICATION: US/09/900,237   TIME: 10:13:55

Input Set : A:\BB1170 US CIP Seq Listing.txt
Output Set: N:\CRF3\07242001\I900237.raw

```
62                 20                      25                      30
64 Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly
65            35                  40                  45
67 Ser Val Glu Ile Leu Phe Ser Arg His Cys Pro Ile Trp Tyr Asn Tyr
68       50                  55                  60
70 Gly Gly Arg Leu Lys Leu Leu Glu Arg Met Ala Tyr Ile Asn Thr Ile
71  65                  70                  75                  80
73 Val Tyr Pro Ile Thr Ser Leu Pro Leu Ile Ala Tyr Cys Val Leu Pro
74                85                  90                  95
76 Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile Ser Asn
77            100                 105                 110 .
79 Tyr Ala Gly Met Phe Phe Ile Leu Met Phe Ala Ser Ile Phe Ala Thr
80       115                 120                 125
82 Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp Trp Trp
83       130                 135                 140
85 Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His Leu Phe
86 145                 150                 155                 160
88 Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn
89            165                 170                 175
91 Phe Thr Val Thr Ser Lys Ala Asn Asp Glu Asp Gly Asp Phe Ala Glu
92            180                 185                 190
94 Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr Thr Val
95       195                 200                 205
97 Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr Ala Ile
98    210                 215                 220
100 Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe
101 225                 230                 235                 240
103 Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly Leu Met
104            245                 250                 255
106 Gly Lys Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu
107            260                 265                 270
109 Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro Phe Ile
110       275                 280                 285
112 Ser Asp Thr Gln Lys Ala Val Ala Met Gly Gln Cys Gly Val Asn Cys
113       290                 295                 300
115 <210> SEQ ID NO: 3
116 <211> LENGTH: 3776
117 <212> TYPE: DNA
118 <213> ORGANISM: Zea mays
120 <400> SEQUENCE: 3
121 gcgcgccgcg caggcgcaac gcaacaaagg gaaaccccag ccggaggagc aaaagctagc    60
122 aagcgtgtcc ctccccctcc ctcactcccg tttcattcca ttcccccca dacgccgcta   120
123 ccgccgccgc cgcacgcacg cttgccccgg gatctggaga tctggtagcg ccagggggat   180
124 ggaggccagc gccgggctgg tcgccggctc gcacaaccgg aacgagctcg tcgtcatccg   240
125 ccgcgatggc gagccagggc cgaagcccat ggaccagcgg aacggccagg tgtgccagat   300
126 ttgcggcgac gacgtggggc gcaaccccga cggggagccg ttcgtggcct gcaacgagtg   360
127 cgccttcccc atctgccggg actgctacga gtacgagcgc cgcgagggca cgcagaactg   420
128 cccccagtgc aagacccgct tcaagcgcct caaggggtgc gcgcgcgtgc ccggggacga   480
129 ggaggaggac ggcgtcgacg acctggagaa cgagttcaac tggagcgaca agcacgactc   540
```

RAW SEQUENCE LISTING   DATE: 07/24/2001
PATENT APPLICATION: US/09/900,237   TIME: 10:13:55

Input Set : A:\BB1170 US CIP Seq Listing.txt
Output Set: N:\CRF3\07242001\I900237.raw

```
130 ccagtacctc gccgagtcca tgctccacgc ccacatgagc tacggccgcg gcgccgacct  600
131 cgacggcgtg ccgcagccat tccaccccat ccccaatgtt cccctcctca ccaacggaca  660
132 gatggtcgat gacatcccgc cggaccagca cgcccttgtg ccctcgttcg tgggtggcgg  720
133 ggggaagagg attcaccctc tcccgtacgc ggatcccaac cttcctgtgc aaccgaggtc  780
134 tatggaccct tccaaggatc tcgccgcata tggctacggg agcgtagcat ggaaggagag  840
135 gatggagagc tggaagcaga agcaggagag gatgcaccag acgaggaacg atggcggcgg  900
136 cgatgatggt gatgatgcag atctaccact aatggatgaa gctagacagc cattgtccag  960
137 aaagatcccg cttccttcaa gccaaatcaa cccctatagg atgattataa taattcggct 1020
138 agtggttttg tgtttcttct tccactaccg agtgatgcat ccggtgcctg atgcatttgc 1080
139 tttatggctc atatctgtga tctgtgaaat ttggtttgcc atgtcttgga ttcttgacca 1140
140 gtttccaaag tggtttccta tcgagaggga aacctatctt gaccggctga gtttaaggtt 1200
141 tgacaaggaa gggcatcctc ctcaactcgc ccctgttgat ttctttgtca gtacggttga 1260
142 tcccttgaag gaacctccat tggtcactgc taatactgtt ctatctatcc tttcggtgga 1320
143 ttatccagtt gataaggttt catgctacgt ttctgatgat ggtgctgcca tgctgacatt 1380
144 tgaagcattg tctgaaacat ctgaatttgc aaagaaatgg gttcctttct gcaaaagata 1440
145 tagccttgag cctcgtgctc cagagtggta cttccaacag aagatagact acctgaaaga 1500
146 caaggtggcg ccaaactttg ttagagaacg gagagcaatg aagagagagt atgaggaatt 1560
147 caaggtcaga atcaatgcct tggttgctaa agcccaaaag gttcctgagg aaggatggac 1620
148 aatgcaggat ggaactccat ggcccggaaa taatgtccgt gatcatcctg gaatgattca 1680
149 ggttttcctt ggtcaaagtg gtggccatga tgtggaagga aatgagctgc ctcgattggt 1740
150 ttatgtttca agagaaaaac ggccaggcta caaccatcac aagaaggctg gtgctatgaa 1800
151 tgcattggtc cgagtctctg ctgtactaac taatgctcct tatttgctga acttggattg 1860
152 tgatcactat atcaataata gtaaggctat aaaggaagca atgtgtttta tgatggatcc 1920
153 tttgcttgga aagaaagttt gctatgtgca gtttcctcaa agatttgatg ggattgatcg 1980
154 ccatgatcga tatgctaaca gaaatgttgt ctttttcgat atcaacatga aaggtttgga 2040
155 tggtatccag ggcccaattt atgtgtgggac tggatgtgtc ttcagaaggc aggcattata 2100
156 tggctacgat gctcccaaaa caaagaagcc accatcaaga acttgcaact gctggccaaa 2160
157 gtggtgcatt tgctgttgct gttttggtaa caggaagacc aagaagaaga ccaagacctc 2220
158 taaacctaaa tttgagaaga taaagaaact ttttaagaaa aaggaaaatc aagcccctgc 2280
159 atatgctctt ggtgaaattg atgaagccgc tccaggagct gaaaatgaaa aggctagtat 2340
160 tgtaaatcaa cagaagttgg aaaagaaatt tggccagtct tcagtttttg ttgcatccac 2400
161 acttcttgag aatggtggaa ccctgaagag tgccagtcca gcttctcttc tgaaggaagc 2460
162 tatacatgtc atcagttgtg gatatgaaga caaaacaggc tggggaaaag atattggttg 2520
163 gatttatgga tcagtcacag aagatattct tactgggttt aagatgcact gccatggttg 2580
164 gcggtcaatt tactgcatac ctaaacgggc cgccttcaaa ggttccgcac ctctcaatct 2640
165 ttccgatcgt cttcaccagg ttcttcggtg ggctcttggt tcaattgaaa ttttcttcag 2700
166 caaccactgc cctctctggt atgggtatgg tggtggacta aagttcctgg aaaggttttc 2760
167 gtacattaac tccatcgtat acccttggac atctatcccg ctcttggcct attgcacatt 2820
168 gcctgccatc tgcttgctga cagggaaatt tatcacgcca gagcttaaca atgttgccag 2880
169 cctctggttc atgtcacttt tcatctgcat ttttgctacg agcatcctgg aaatgagatg 2940
170 gagtggtgta ggcatcgatg actggtggag aaacgagcag ttttgggtca ttggaggcgt 3000
171 gtcttcacat ctctttgctg tgttccaggg actcctcaag gtcatagctg gtgtagacac 3060
172 gagcttcact gtgacatcca agggcggaga cgacgaggag ttctcagagc tgtacacatt 3120
173 caaatggacg acccttctga tacctccgac aaccctgctc ctactgaact tcattggagt 3180
174 ggtagctggc atctccaatg cgatcaacaa cggatatgaa tcatggggcc ccctgttcgg 3240
175 gaagctcttc tttgcatttt gggtgatcgt ccatctttac ccgttcctca agggtctggt 3300
176 tgggaggcag aacaggacgc caacgattgt cattgtctgg tccatcctcc tggcttcgat 3360
177 cttctcgctg ctttgggtcc ggatcgaccc gttccttgcg aaggatgatg gtcccctgtt 3420
178 ggaggagtgt ggtctggatt gcaactagga ggtcagcacg tggacttccc cgtcagtgtg 3480
```

```
179 tggtcgaaga agtatttttg cagatgtttt gtgcccatat ttcttttttc aatttttgtc 3540
180 cctctgtaga tagaaacaag gggagaaggg gaaaaaaagt acttgtattt cttttgttcc 3600
181 atggtggtgg tggtggtggg cggctcagcc tcgtgagtgc agtattgggc aaaccggagg 3660
182 ctgcggcaac cttgtgcagt tcggccacga atatactagg gaagatcgcg accaatcaat 3720
183 caatcgatga ccgagttcaa ttgttcagca ·aaaaaaaaaa aaaaaaaaaa aaaaaa     3776
185 <210> SEQ ID NO: 4
186 <211> LENGTH: 1148
187 <212> TYPE: PRT
188 <213> ORGANISM: Zea mays
190 <400> SEQUENCE: 4
191 Arg Ala Ala Gln Ala Gln Arg Asn Lys Gly Lys Pro Gln Pro Glu Glu
192  1               5                  10                  15
194 Gln Lys Leu Ala Ser Val Ser Leu Pro Leu Pro His Ser Arg Phe Ile
195             20                  25                  30
197 Pro Phe Pro Pro Arg Arg Arg Tyr Arg Arg Arg Arg Thr His Ala Cys
198             35                  40                  45
200 Pro Gly Ile Trp Arg Ser Gly Ser Ala Arg Gly Met Glu Ala Ser Ala
201      50                  55                  60
203 Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg
204  65                  70                  75                  80
206 Arg Asp Gly Glu Pro Gly Pro Lys Pro Met Asp Gln Arg Asn Gly Gln
207             85                  90                  95
209 Val Cys Gln Ile Cys Gly Asp Asp Val Gly Arg Asn Pro Asp Gly Glu
210             100                 105                 110
212 Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro Ile Cys Arg Asp Cys
213             115                 120                 125
215 Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn Cys Pro Gln Cys Lys
216      130                 135                 140
218 Thr Arg Phe Lys Arg Leu Lys Gly Cys Ala Arg Val Pro Gly Asp Glu
219 145                 150                 155                 160
221 Glu Glu Asp Gly Val Asp Asp Leu Glu Asn Glu Phe Asn Trp Ser Asp
222             165                 170 .               175
224 Lys His Asp Ser Gln Tyr Leu Ala Glu Ser Met Leu His Ala His Met
225             ·180                185 .               190
227 Ser Tyr Gly Arg Gly Ala Asp Leu Asp Gly Val Pro Gln Pro Phe His
228      195                 200                 205
230 Pro Ile Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp
231      210                 215                 220
233 Ile Pro Pro Asp Gln His Ala Leu Val Pro Ser Phe Val Gly Gly Gly
234 225                 230                 235                 240
236 Gly Lys Arg Ile His Pro Leu Pro Tyr Ala Asp Pro Asn Leu Pro Val
237             245                 250                 255
239 Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr
240             260                 265                 270
242 Gly Ser Val Ala Trp Lys Glu Arg Met Glu Ser Trp Lys Gln Lys Gln
243      275                 280                 285
245 Glu Arg Met His Gln Thr Arg Asn Asp Gly Gly Gly Asp Asp Gly Asp
246      290                 295                 300
248 Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg
```

```
249 305                   310              315              320
251 Lys Ile Pro Leu Pro Ser Ser Gln Ile Asn Pro Tyr Arg Met Ile Ile
252               325              330              335
254 Ile Ile Arg Leu Val Val Leu Cys Phe Phe Phe His Tyr Arg Val Met
255               340              345              350
257 His Pro Val Pro Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys
258               355              360              365
260 Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp
261       370              375              380
263 Phe Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe
264 385              390              395              400
266 Asp Lys Glu Gly His Pro Ser Gln Leu Ala Pro Val Asp Phe Phe Val
267               405              410              415
269 Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn Thr
270               420              425              430
272 Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val Ser Cys
273               435              440              445
275 Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu Ser
276       450              455              460
278 Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe Cys Lys Arg Tyr
279 465              470              475              480
281 Ser Leu Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp
282               485              490              495
284 Tyr Leu Lys Asp Lys Val Ala Pro Asn Phe Val Arg Glu Arg Arg Ala
285               500              505              510
287 Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val
288       515              520              525
290 Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Gln Asp Gly
291       530              535              540
293 Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro Gly Met Ile Gln
294 545              550              555              560
296 Val Phe Leu Gly Gln Ser Gly Gly His Asp Val Glu Gly Asn Glu Leu
297               565              570              575
299 Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Asn His
300               580              585              590
302 His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val
303       595              600              605
305 Leu Thr Asn Ala Pro Tyr Leu Leu Asn Leu Asp Cys Asp His Tyr Ile
306       610              615              620
308 Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe Met Met Asp Pro
309 625              630              635              640
311 Leu Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp
312               645              650              655
314 Gly Ile Asp Arg His Asp Arg Tyr Ala Asn Arg Asn Val Val Phe Phe
315               660              665              670
317 Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Ile Tyr Val
318       675              680              685
320 Gly Thr Gly Cys Val Phe Arg Arg Gln Ala Leu Tyr Gly Tyr Asp Ala
321       690              695              700
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/900,237**

DATE: 07/24/2001
TIME: 10:13:56

Input Set : **A:\BB1170 US CIP Seq Listing.txt**
Output Set: **N:\CRF3\07242001\I900237.raw**

```
L:8 M:270 C: Current Application Number differs, Replaced Application Number
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1289 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:1289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1841 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1841 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1893 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
```